Fig. 1

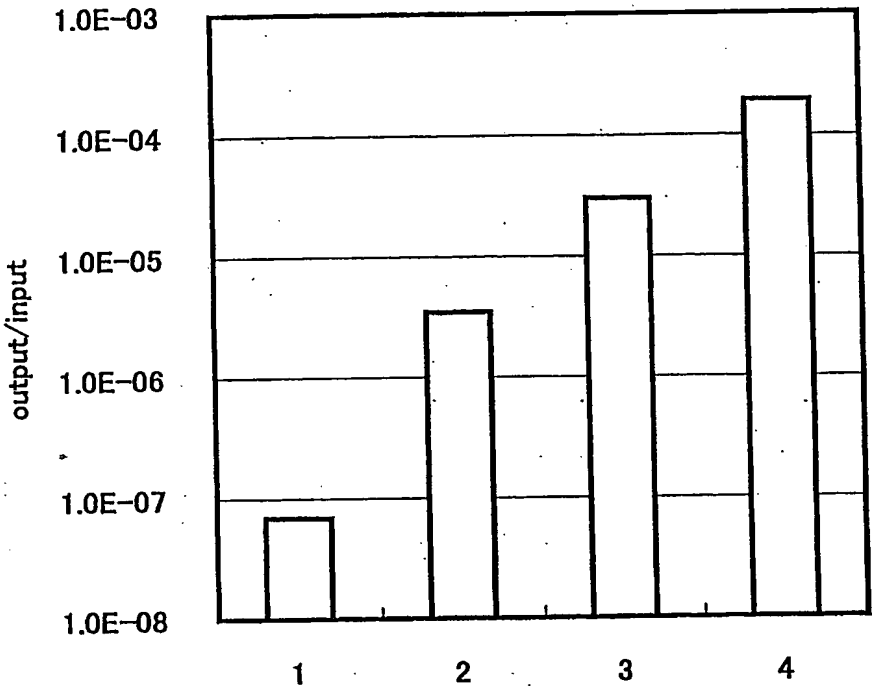


Fig. 2

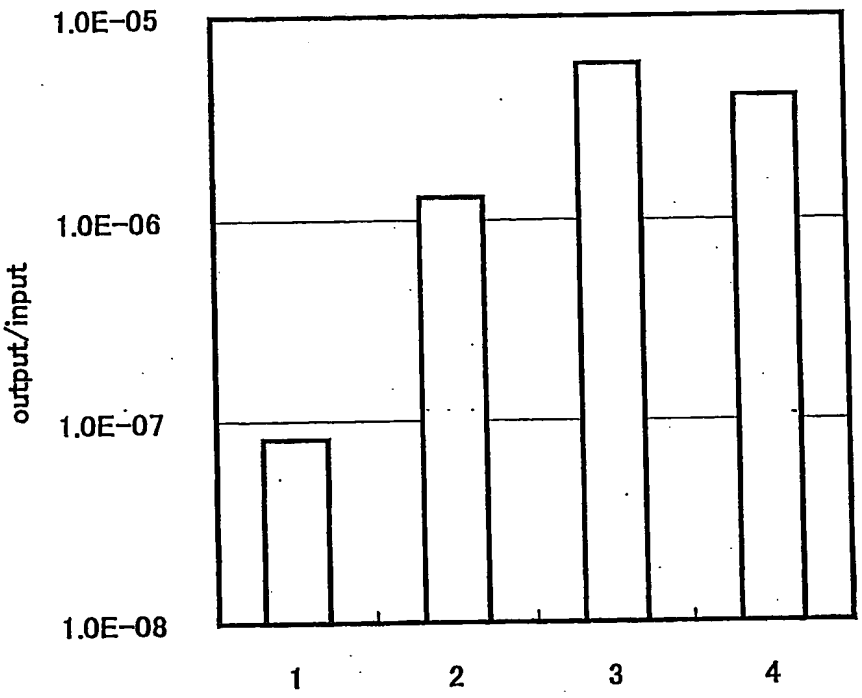


Fig. 3

e3-2-2	LDTTNVSGPMSS
e3-2-3	RKLPDAPGMHTW
e3-2-4	RKLPDAPGMHTW
e3-2-5	SYRLPVYLHALL
e3-2-6	RKLPDAPGMHTW
e3-2-7	RKLPDAPGMHTW
e3-2-8	SDPNQDWRRTTP
e3-2-9	RKLPDAPGMHTW
e3-2-10	RKLPDAPGMHTW
e3-2-12	LPSQLLSQVNLT
e3-2-13	RKLPDAPGMHTW
e3-2-14	RKLPDAPGMHTW
e3-2-15	RKLPDAPGMHTW
e3-2-16	RKLPDAPGMHTW
e3-2-17	RKLPDAPGMHTW
e3-2-18	RKLPDAPGMHTW
e3-2-19	LCANNTTSVHPP
e3-2-20	RKLPDAPGMHTW
e3-2-21	MQMEGKPTLTLR
e3-2-22	RKLPDAPGMHTW
e3-2-23	RKLPDAPGMHTW
e3-2-25	RKLPDAPGMHTW
e3-2-29	STLKNPINLLAN
e3-2-30	RKLPDAPGMHTW
e3-2-31	RKLPDAPGMHTW
e3-2-33	RKLPDAPGMHTW
e3-2-34	RKLPDAPGMHTW
e3-2-36	RKLPDAPGMHTW
e3-2-39	RKLPDAPGMHTW
e3-2-40	RKLPDAPGMHTW
e3-2-41	RKLPDAPGMHTW
e3-2-42	RKLPDAPGMHTW
e3-2-43	SCHVWYDSCSSP
e3-2-45	RKLPDAPGMHTW
e3-2-46	RKLPDAPGMHTW
e3-2-47	RKLPDAPGMHTW
e3-2-48	RKLPDAPGMHTW
e3-2-49	RKLPDAPGMHTW
e3-2-50	STLKNPINLLAN
e3-2-51	RKLPDAPGMHTW
e3-2-52	RKLPDAPGMHTW
e3-2-55	QDMIRTSALMLQ
e3-2-56	RKLPDAPGMHTW

Fig. 4

e3-4-2	CTSPTSVDC
e3-4-3	CTPSPHQGC
e3-4-4	CHTAPLPRC
e3-4-5	CTPSPHQGC
e3-4-6	CHGATPQNC
e3-4-7	CSGHNPTHC
e3-4-8	CTSPTSVDC
e3-4-9	CTPSPHQGC
e3-4-11	CPMWQAQQC
e3-4-12	CGYYSMSHC
e3-4-13	CDMLTPRSC
e3-4-15	CTSPTSVDC
e3-4-16	CLRLQSQDC
e3-4-17	CQITWHHTC
e3-4-19	CTPSPHQGC
e3-4-21	CSAHHHDKC
e3-4-22	CTPSPHQGC
e3-4-23	CMTKNPLNC
e3-4-24	CTPSPHQGC
e3-4-25	CTPSPHQGC
e3-4-26	CTPSPHQGC
e3-4-27	CTSPTSVDC
e3-4-28	CMTKNPLNC
e3-4-29	CKTSLPTTC
e3-4-30	CVSTYWKTC
e3-4-31	CTSPTSVDC
e3-4-32	CTSPTSVDC

Fig. 5

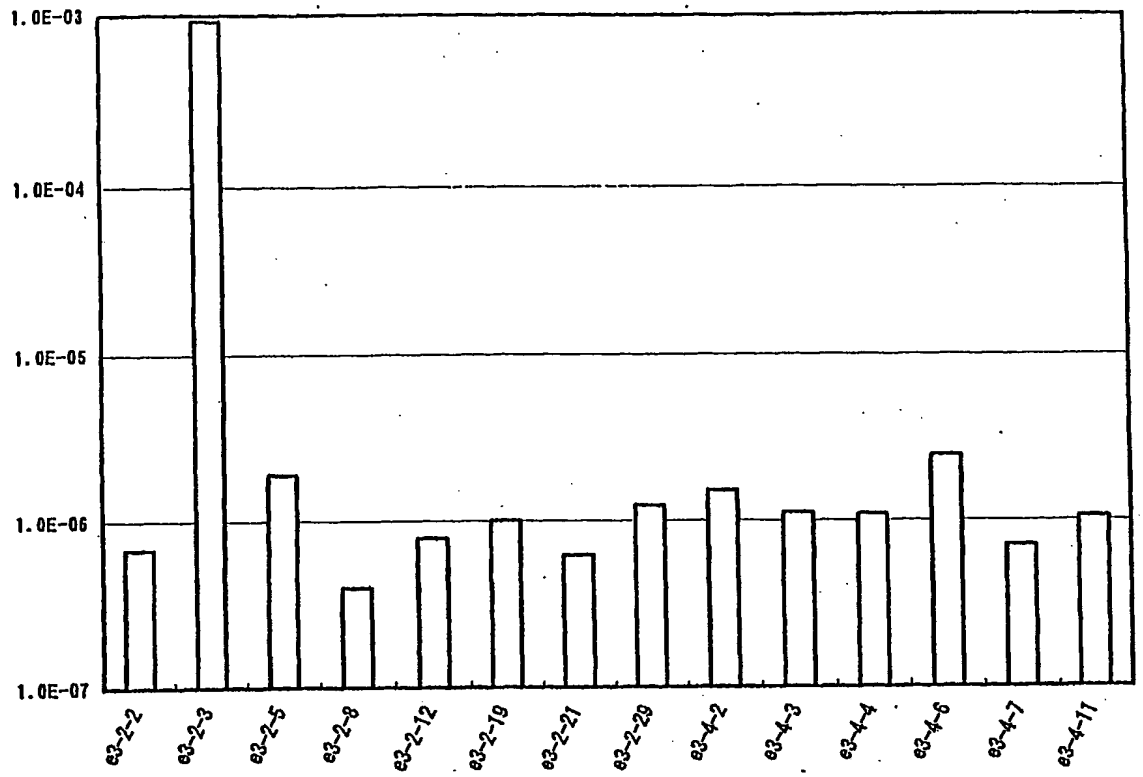
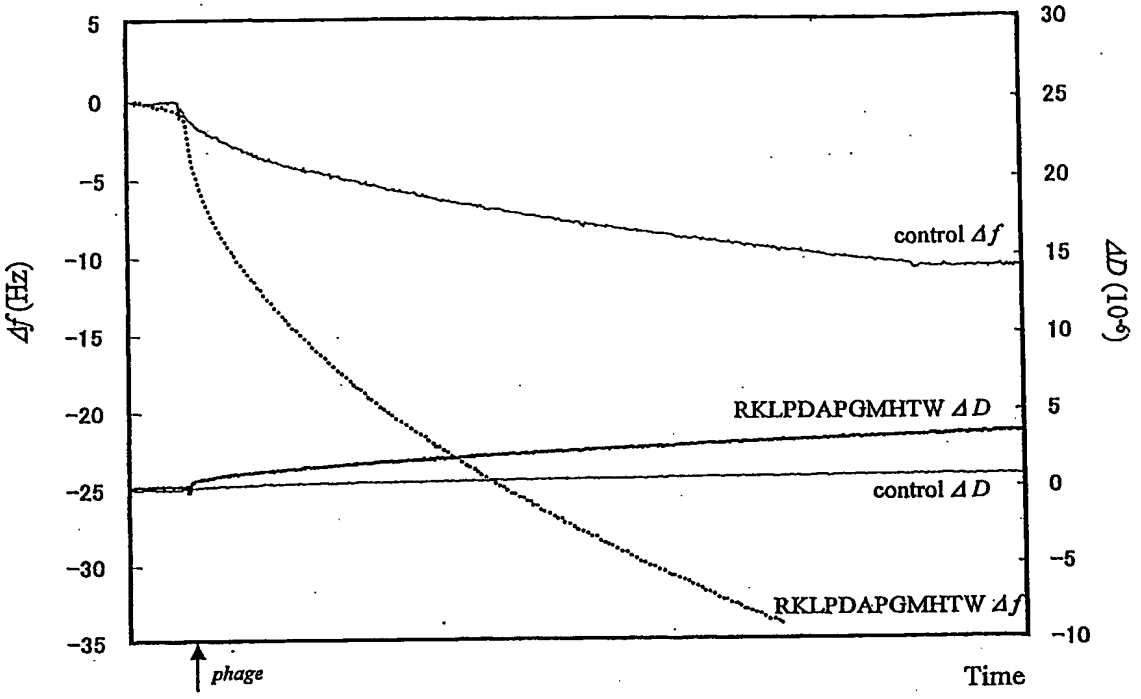

1.0E-03
1.0E-04
1.0E-05
1.0E-06
1.0E-07
e3-2-2
e3-2-3
e3-2-5
e3-2-8
e3-2-12
e3-2-19
e3-2-21
e3-2-29
e3-4-2
e3-4-3
e3-4-4
e3-4-6
e3-4-7
e3-4-11

Fig. 6

A: Non-blocking



B: BSA blocking

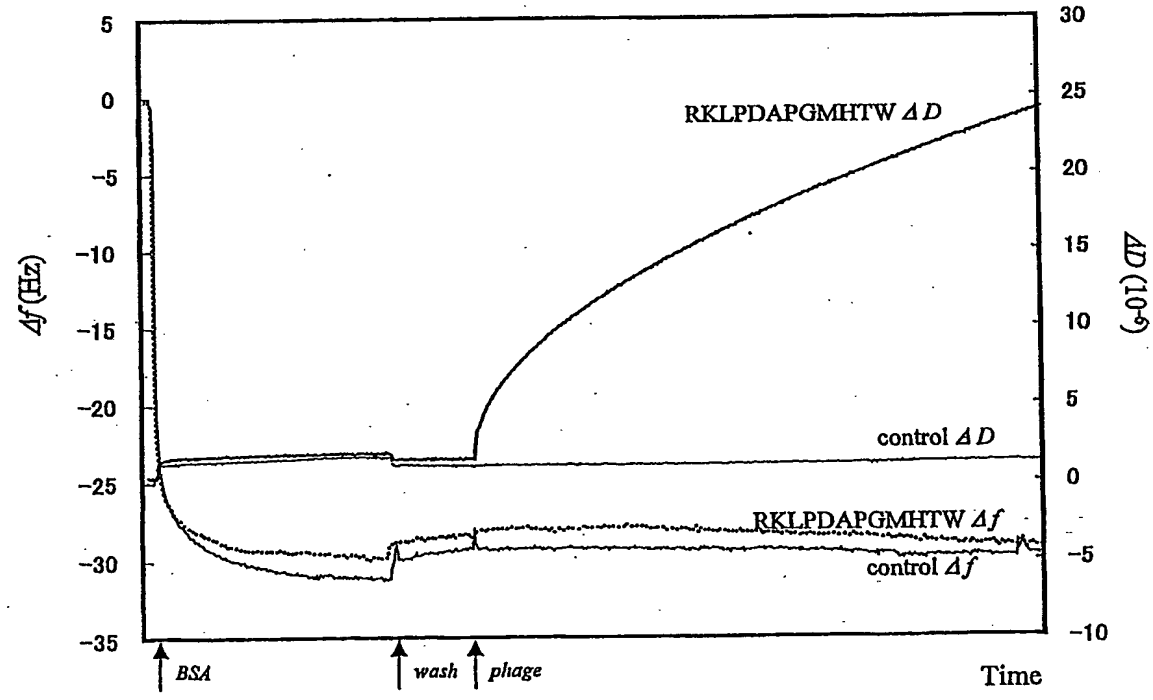
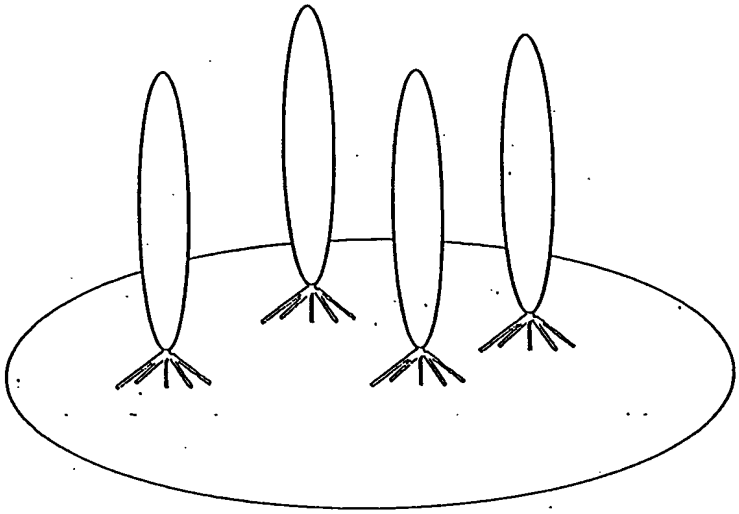


Fig. 7



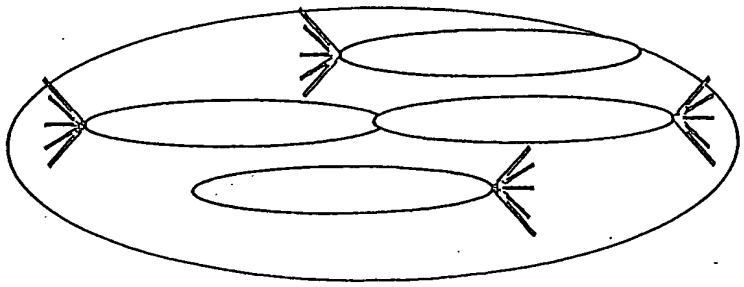


Fig. 8

R1A: AGGCAGCTTCGCAGAGTGAGAATAG

K2A: CATCAGGCAGCGCCCGAGAGTGAG

L3A: GGAGCATCAGGCGCCTTCCGAGAG

P4A: CCGGGAGCATCAGCCAGCTTCCGAG

D5A: ATCCCGGGAGCAGCAGGCAGCTTC

P7A: GTATGCATCCCGGCAGCATCAGGCA

G8A: AGTATGCATCGCGGGAGCATCAGG

M9A: CCCCAAGTATGCGCCCCGGGAGCATC

H10A: TCCACCCCAAGTAGCCATCCCGGGA

T11A: TCCACCCCAAGCATGCATCCCGG

W12A: AACCTCCACCCGCAGTATGCATC

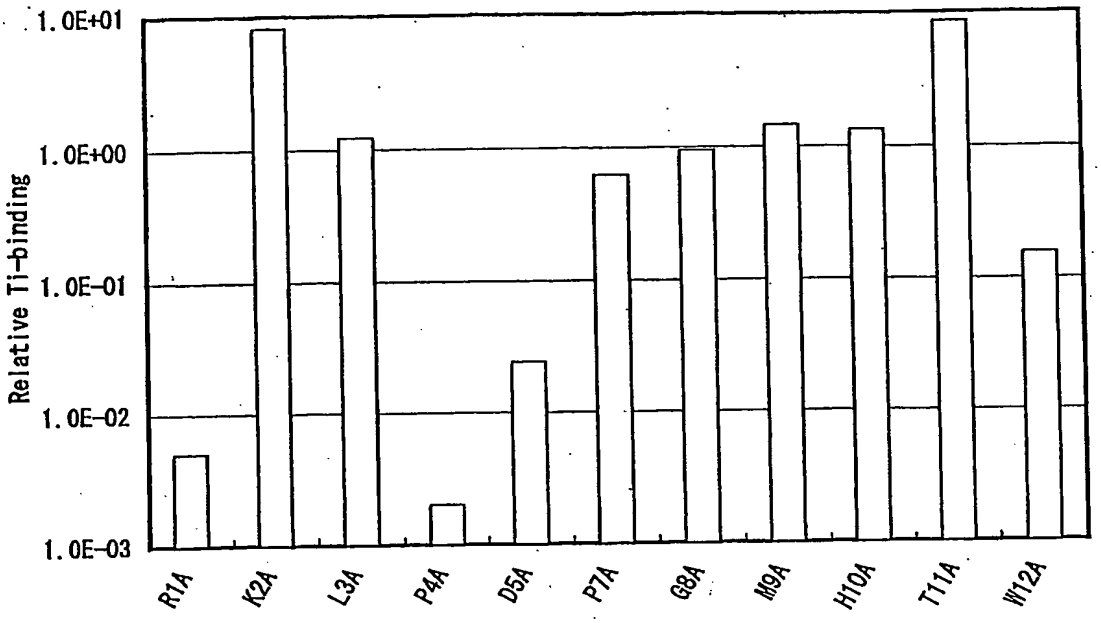
Δ7-12F; GGAGGATCCGCCGAAACTGTTGAAAGTTG

Δ7-12R; GGGGGATCCTCCACCAGCATCAGGCAGCTTCCGAG

K2AΔ7-12R; GGGGGATCCTCCACCAGCATCAGGCAGCGCCCGAG

Ala insert; AGCATCAGGCAGCTTCCGTGCAGAGTGAGAATAGAAAGG

Fig. 9


Relative Ti-binding
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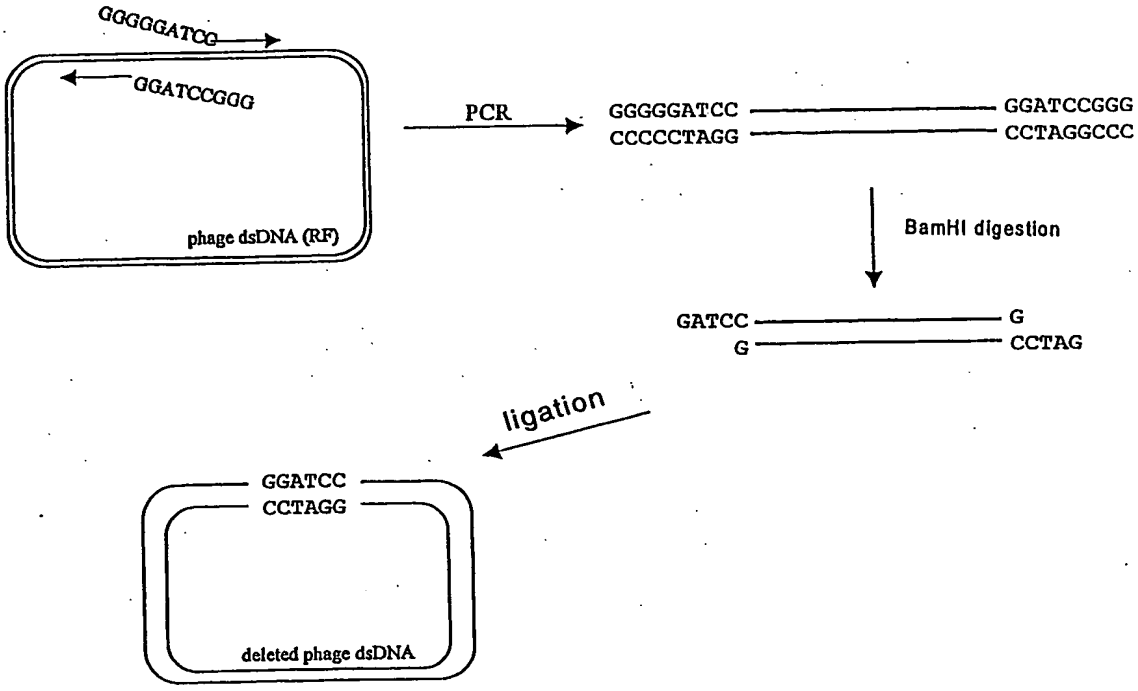
1.0E+00
1.0E-01
1.0E-02
1.0E-03
R1A
K2A
L3A
P4A
D5A
P7A
G8A
M9A
H10A
T11A
W12A

Fig. 10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GGATCCGGG
phage dsDNA (RF)
PCR
GGGGGATCC
CCCCCTAGG
GGATCCGGG
CCTAGGCCC
BamHI digestion
GATCC
G
G
CCTAG
ligation
GGATCC
CCTAGG
deleted phage dsDNA

Fig. 11

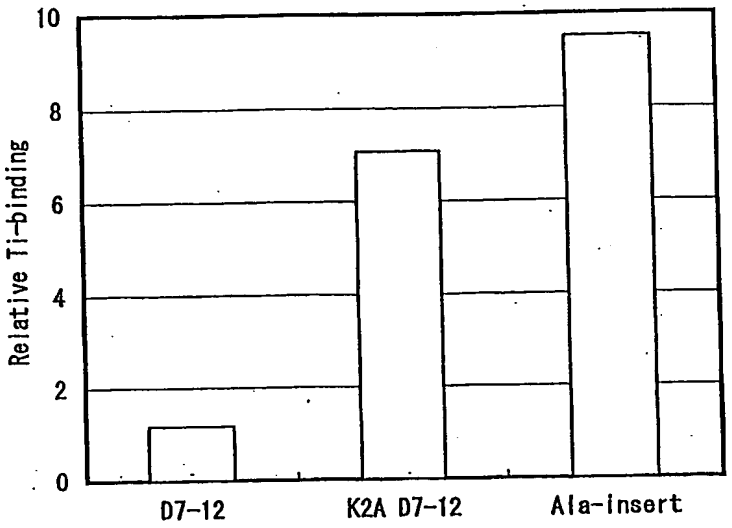


Fig. 12

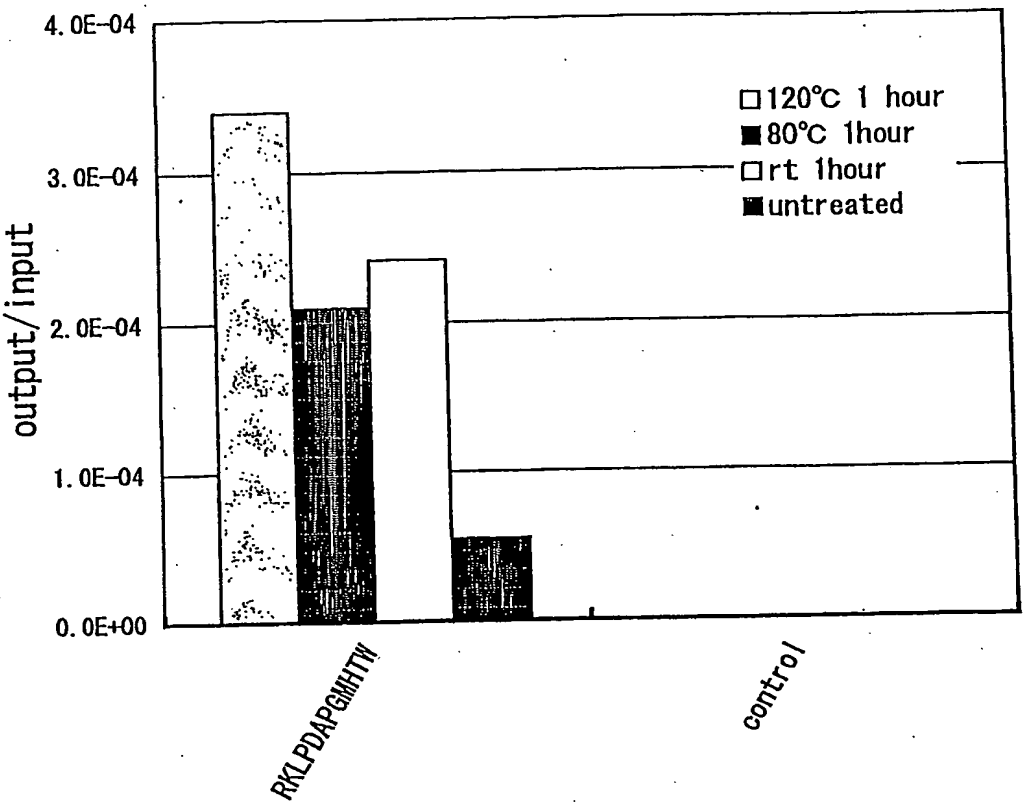

4.0E-04
3.0E-04
2.0E-04
1.0E-04
0.0E+00
output/input
□120℃ 1 hour
■80℃ 1hour
□rt 1hour
■untreated
RKLPDAPGMHTW
control

Fig. 13

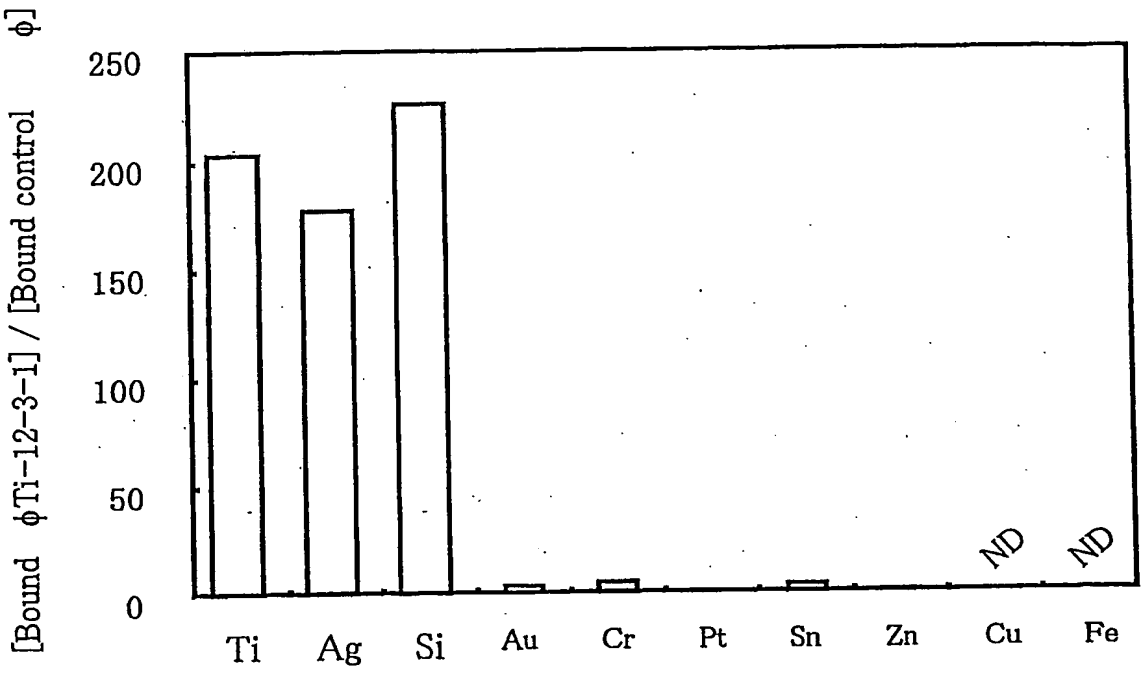

[Bound φTi-12-3-1] / [Bound control φ]
250
200
150
100
50
0
Ti
Ag
Si
Au
Cr
Pt
Sn
Zn
Cu
Fe
ND
ND

Fig. 14

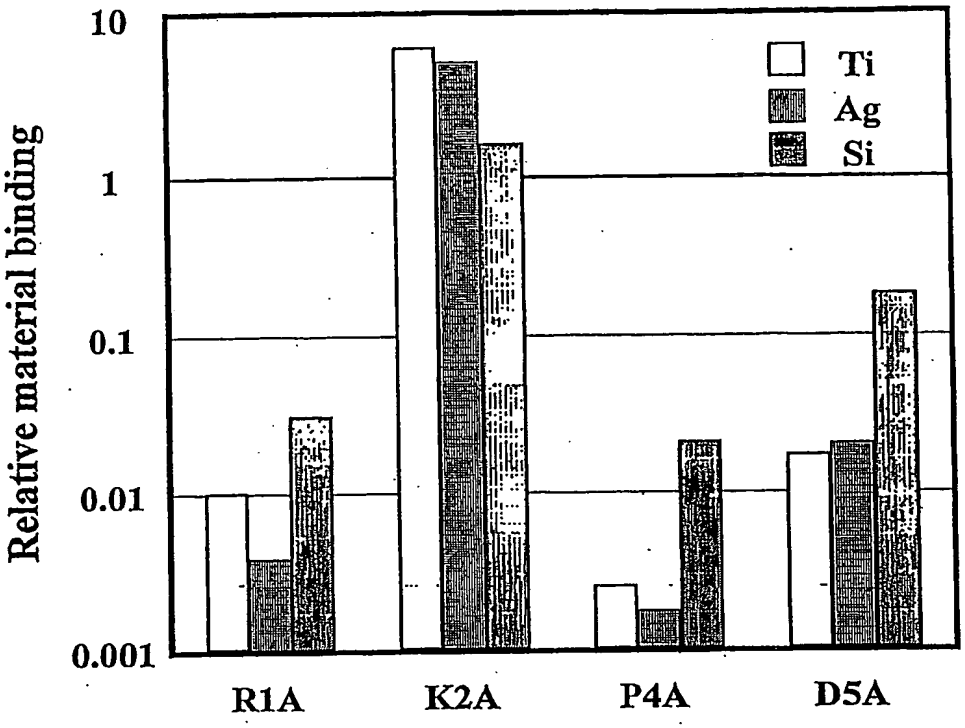
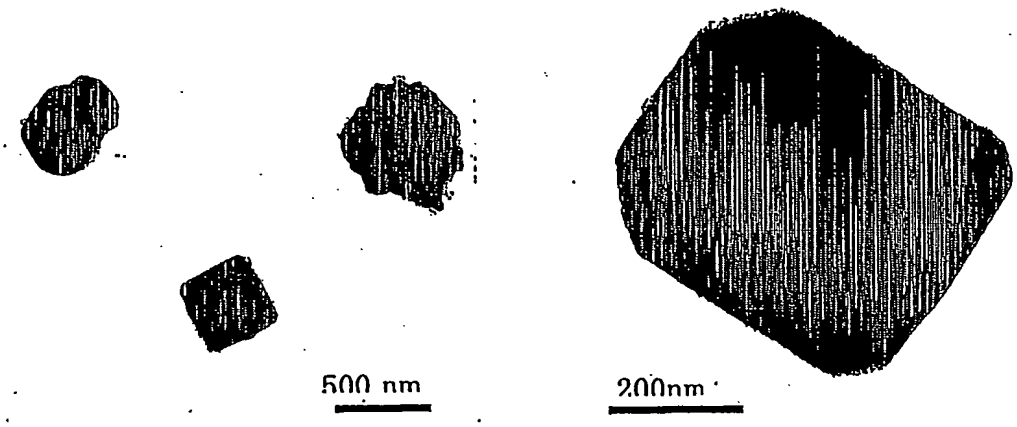

Relative material binding
10
1
0.1
0.01
0.001
Ti
Ag
Si
R1A
K2A
P4A
D5A

Fig. 15



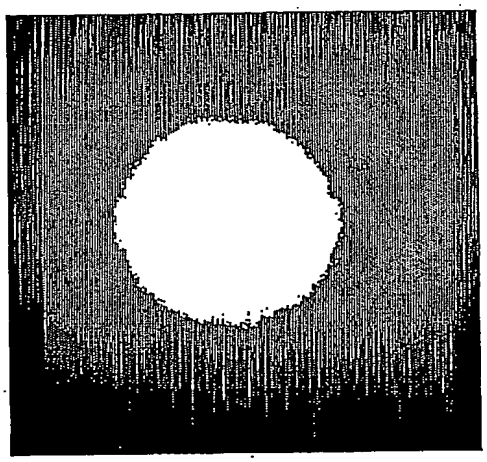


Fig. 16

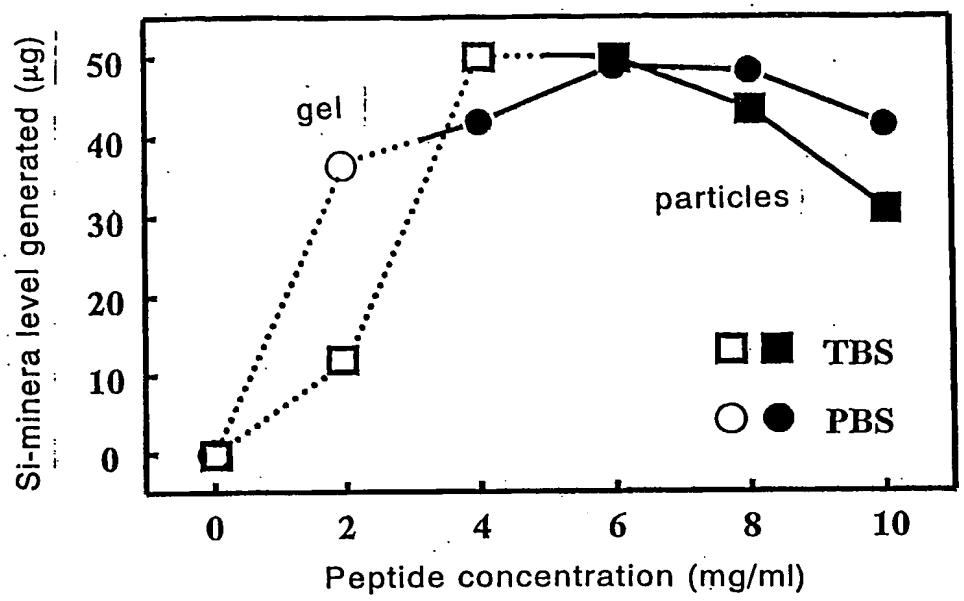

Si-minera level generated (μg)
50
40
30
20
10
0
gel
particles
TBS
PBS
0
2
4
6
8
10
Peptide concentration (mg/ml)

Fig. 17

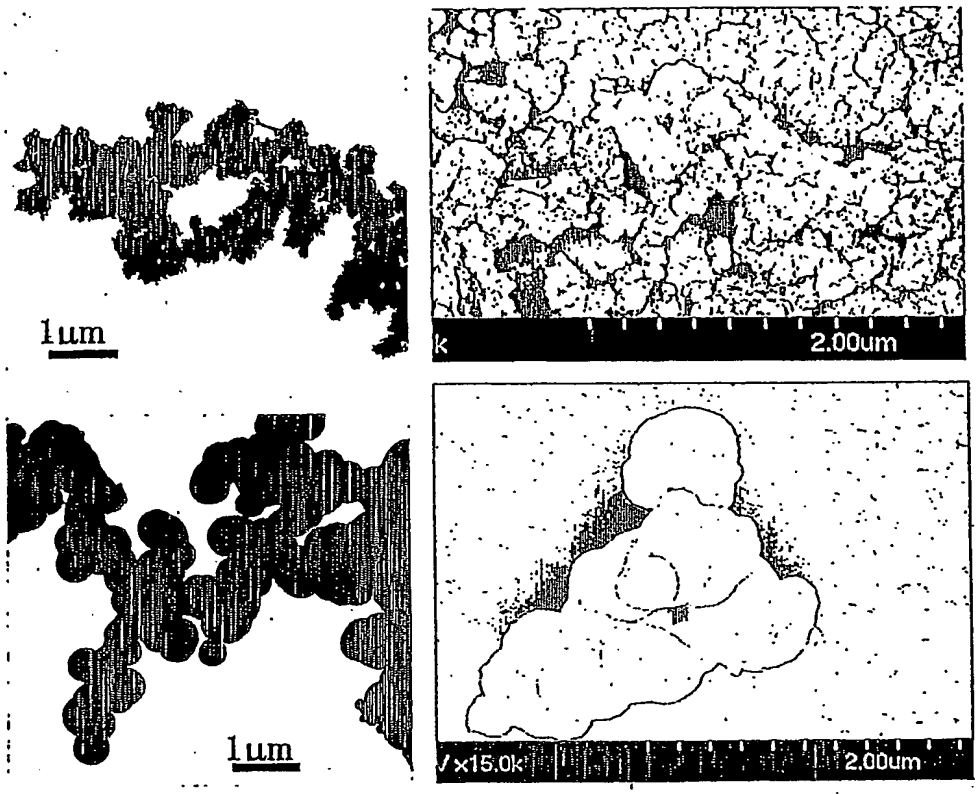
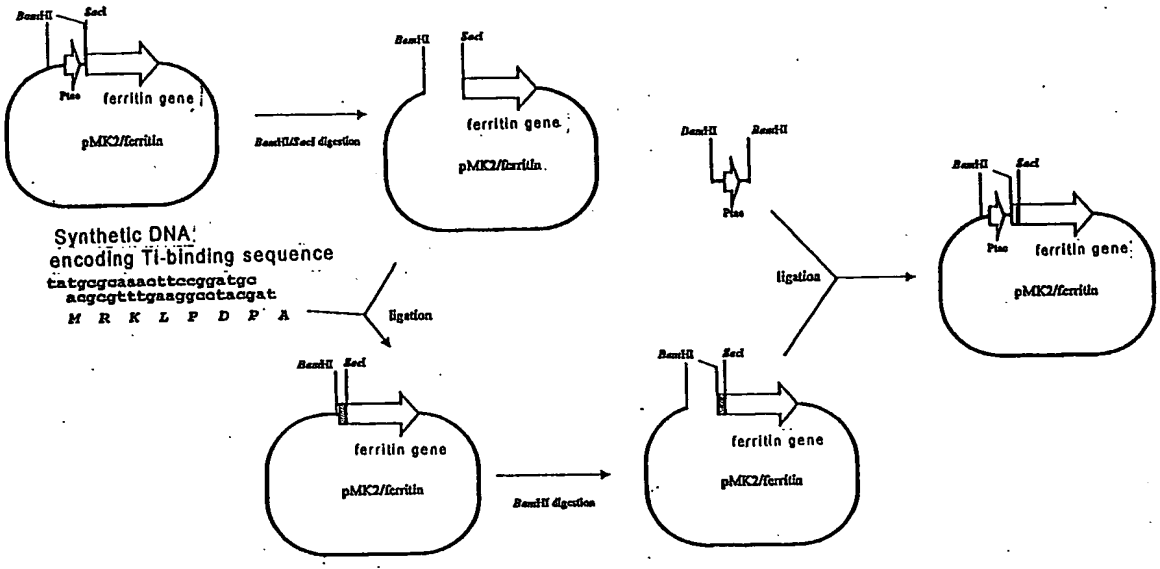


Fig. 18


BamHI
SacI
PtacI
ferritin gene
pMK2/ferritin
BamHI/SacI digestion
Synthetic DNA
encoding Ti-binding sequence
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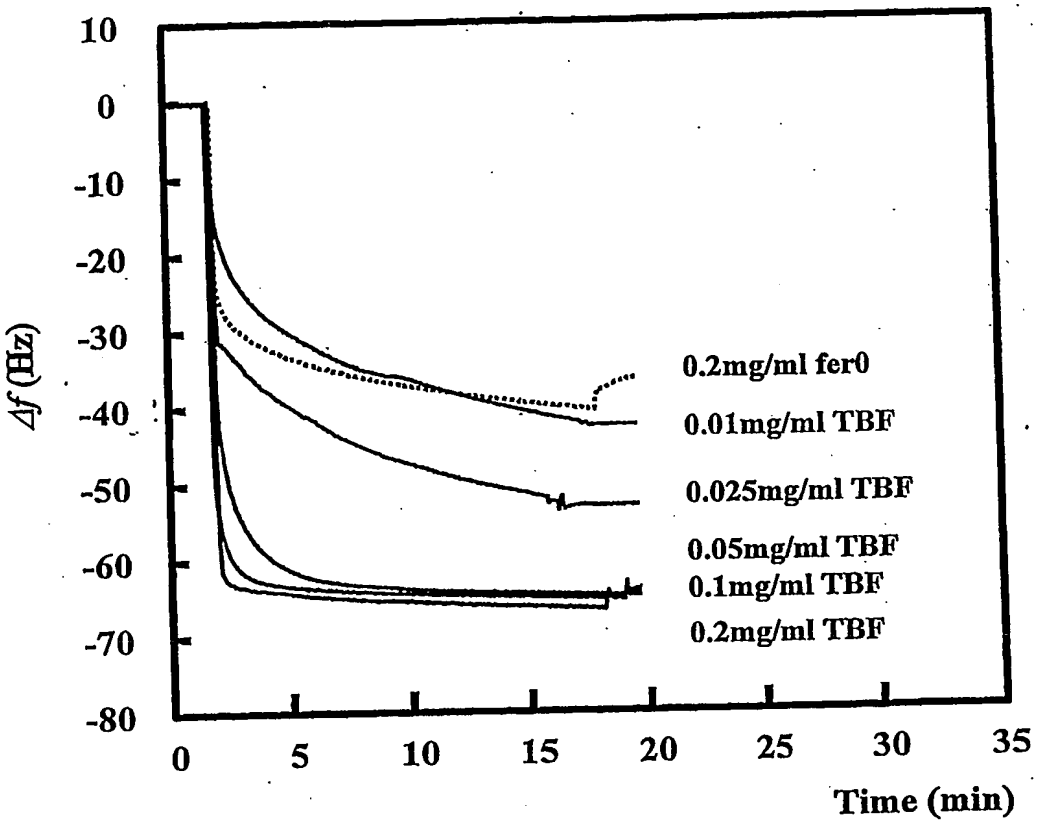
aagcgtttgaaggcctacgat
M R K L P D P A
ligation
BamHI digestion

Fig. 19


10
0
-10
-20
-30
-40
-50
-60
-70
-80
Δf (Hz)
0
5
10
15
20
25
30
35
Time (min)
0.2mg/ml fer0
0.01mg/ml TBF
0.025mg/ml TBF
0.05mg/ml TBF
0.1mg/ml TBF
0.2mg/ml TBF